

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:32:48 ; Search time 1275.67 Seconds
(without alignments)
386.247 Million cell updates/sec

Title: US-09-581-528E-20

Perfect score: 1 tGtGtCGGgATGATyGcCvVcAcTgGaaAgGCC 36

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 25053377 seqs, 6843368929 residues

Total number of hits satisfying chosen parameters: 50106754

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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26: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	33.2	92.2	36	6	US-09-581-528E-19
5	33.2	92.2	36	6	US-09-581-528E-20
6	32.4	90.0	1404	6	US-09-581-528E-4
7	32.4	90.0	1929	24	US-11-070-405-3

8	32.4	90.0	1964	24	US-11-070-405-135	Sequence 135, App
9	31.6	87.8	1407	2	PCT-US04-42360-2316	Sequence 2316, App
10	31.6	87.8	1407	24	US-11-136-527-2454	Sequence 2454, App
11	26	72.2	201	26	US-60-659-397-5930	Sequence 5930, App
12	26	72.2	201	26	US-60-659-397-6011	Sequence 6011, App
13	26	72.2	201	26	US-60-659-397-6090	Sequence 6090, App
14	26	72.2	201	26	US-60-659-397-27095	Sequence 27095, App
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22	25.2	70.0	201	26	US-60-659-397-6013	Sequence 6013, App
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26	25.2	70.0	201	26	US-60-659-397-6089	Sequence 6089, App
27	25.2	70.0	201	26	US-60-659-397-6091	Sequence 6091, App
28	25.2	70.0	201	26	US-60-659-397-6092	Sequence 6092, App
29	25.2	70.0	201	26	US-60-659-397-6093	Sequence 6093, App
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39	25.2	70.0	469	24	US-11-070-405-63	Sequence 63, App1
40	25.2	70.0	489	24	US-11-070-405-74	Sequence 74, App1
41	25.2	70.0	498	24	US-11-070-405-62	Sequence 62, App1
42	25.2	70.0	500	24	US-11-070-405-108	Sequence 108, App1
43	25.2	70.0	945	24	US-11-070-405-6	Sequence 6, App1
44	25.2	70.0	945	24	US-11-070-405-160	Sequence 160, App1
45	25.2	70.0	1404	6	US-09-581-528E-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-581-528E-7
Sequence 7, Application US/09581528E
GENERAL INFORMATION:
APPLICANT: TAKEDA, Masatoshi
TITLE OF INVENTION: Gene Mutant Animals
FILE REFERENCE: P19743
CURRENT APPLICATION NUMBER: US/09/581,528E
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: PCT/JP99/00015
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: Primer
US-09-581-528E-7

Query Match 92.2%; Score 33.2; DB 6; Length 36;
Best Local Similarity 88.9%; Pred. No. 0.0013; 0;
Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
DB 1 TGTGTCGGGATGATGCGCCTGGAAGGCC 36
1 TGTGTCGGGATGATGCGCCTGGAAGGCC 36

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:29:14 ; Search time 2455 Seconds

(without alignments)
598.627 Million cell updates/sec

Title: US-09-581-528E-20

Perfect score: 1 tctgtcgcggatgatgycvccvccatcgaaagccc 36

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:33:43 / Search time 362.333 Seconds
(without alignments)
664.322 Million cell updates/sec

Title: US-09-581-528E-20

Perfect score: 1 tctgtcggagatgatygcwvccatcgaagagccc 36

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7400732 seqs, 334317571 residues

Total number of hits satisfying chosen parameters: 14801464

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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C	33	25.2	70.0	121	US-10-681-074-4200	Sequence 4200, Ap
C	34	25.2	70.0	121	US-10-681-074-4201	Sequence 4201, Ap
C	35	25.2	70.0	121	US-10-681-074-4204	Sequence 4204, Ap
C	36	25.2	70.0	121	US-10-681-074-4205	Sequence 4205, Ap
C	37	25.2	70.0	121	US-10-681-074-4208	Sequence 4208, Ap
C	38	25.2	70.0	121	US-10-681-074-4209	Sequence 4209, Ap
C	39	25.2	70.0	121	US-10-681-074-4200	Sequence 4200, Ap
C	40	25.2	70.0	121	US-10-681-074-4201	Sequence 4201, Ap
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C	45	25.2	70.0	121	US-10-681-074-4200	Sequence 4200, Ap

ALIGNMENTS

US-10-957-311-8

Sequence 8, Application US/10957311

Publication No. US20050076400A1

GENERAL INFORMATION:

APPLICANT: CASAS LOUZA, Caty

APPLICANT: BENOIT, Patrick

APPLICANT: PRADIER, Laurent

APPLICANT: TREMP, Gunter

APPLICANT: IITER, Jean-Michel

TITLE OF INVENTION: TRANSGENIC ANIMALS EXHIBITTING MAJOR DISORDERS RELATED TO

FILE REFERENCE: FRAV2003/0027 US NP

CURRENT APPLICATION NUMBER: US/10/957,311

PRIOR FILING DATE: 2004-10-01

PRIOR APPLICATION NUMBER: US 60/523,397

PRIOR FILING DATE: 2003-11-19

PRIOR APPLICATION NUMBER: FR 0311578

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LENGTH: 221

TYPE: DNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Murine PSI Exon 7 Containing Mutations

US-10-957-311-8

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:28:37 ; Search time 69.6667 Seconds
(without alignments)
845.540 Million cell updates/sec

Title: US-09-581-528E-20

Perfect score: 36

Sequence: 1 tgcgtcgagatgatgycvccvccacgtgaaagcc 36

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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 2405568

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C	45	25.2	70.0	500	2 US-08-967-101-108	Sequence 108, App

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Sequence 16, Application US/09544618
Patent No. 6503502

GENERAL INFORMATION:

APPLICANT: Telerman, Adam
APPLICANT: Amson, Robert

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC

FILE REFERENCE: 065691-0139

CURRENT APPLICATION NUMBER: US/09/544,618

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 1636

TYPE: DNA

ORGANISM: MOUSE

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(1636)

OTHER INFORMATION: applicants are unsure of various bases designated as "n"

US-09-544-618-16

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Best Local Similarity 88.9%; Pred. No. 0.00028;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
US-08-967-101-3
Sequence 3, Application US/08967101
Patent No. 5840540

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSER: TESTA, HURWITZ & THIBRAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

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OM nucleic - nucleic search, using SW model

Run on: September 26, 2005, 18:32:48 ; Search time 1275.67 Seconds
(without alignments)
386.247 Million cell updates/sec

Title: US-09-581-528E-19

Perfect score: 36
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ALIGNMENTS

RESULT 1
US-09-581-528E-7
Sequence 7, Application US/09581528E
GENERAL INFORMATION:
APPLICANT: TAKEDA, Junji
TITLE OF INVENTION: Gene Mutant Animals
FILE REFERENCE: P19743
CURRENT FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: PCT/JP99/00015
PRIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: Primer
US-09-581-528E-7

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GenCore version 5.1.6
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Title: US-09-581-528E-19

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; APPLICANT: CASAS LOUZAQ, Cely
; APPLICANT: BENOIT, Patrick
; APPLICANT: PRADIER, Laurent
; APPLICANT: TREMP, Gunter
; APPLICANT: ITIER, Jean-Michel
; APPLICANT: BLANCHARD, Veronique
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXHIBITING MAJOR DISORDERS RELATED TO
; FILE REFERENCE: FRAV2003/0027 US NP
; CURRENT APPLICATION NUMBER: US/10/957,311
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/523,397
; PRIOR FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: FR 0311578
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; OTHER INFORMATION: Murine Psi Exon 7 Containing Mutations
US-10-957-311-8

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OM nucleic - nucleic search, using sw model

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(without alignments)
598.627 Million cell updates/sec

Title: US-09-581-528E-18

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Dp	1	MTEIPAPLSYQNAQMSDSHSSSAISQNDSEERQOQOHRDLNDNEPISNGRPOSNSR	60		
QY	61	QVAVDEDEBDEELTKTGAKHVTMLFVPVTLCAVVVAATIKSVSEFYTRKQGLIYTPETE	120		
Dp	61	QVAVDEDEBDEELTKTGAKHVTMLFVPVTLCAVVVAATIKSVSEFYTRKQGLIYTPETE	120		
QY	121	DTEVVGGRALSHSLNAAIMTSVIVMTLLVLTLYKRCYKVIHAMLLISSLLFFPSFI	180		
Dp	121	DTEVVGGRALSHSLNAAIMTSVIVMTLLVLTLYKRCYKVIHAMLLISSLLFFPSFI	180		
QY	181	YLGEVFPTQVAVADYVTVALLINMFGVGMIALHMGKPLTLOQAVILMISALMAVATIKY	240		
Dp	181	YLGEVFPTQVAVADYVTVALLINMFGVGMIALHMGKPLTLOQAVILMISALMAVATIKY	240		
QY	241	LPFTWAMLLIAVISYVDLVAVILCPKGPLRMLVETAEERNETTLPALITYSSTWMLVMAE	300		
Dp	241	LPFTWAMLLIAVISYVDLVAVILCPKGPLRMLVETAEERNETTLPALITYSSTWMLVMAE	300		
QY	301	GDPEARRRVPKPKNTTORAERTQDGGSGNDGGSSEWEAORDSHLGPHRSTPESRAA	360		
Dp	301	GDPEARRRVPKPKNTTORAERTQDGGSGNDGGSSEWEAORDSHLGPHRSTPESRAA	360		

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OM protein - protein search, using sw model

Run on: September 26, 2005, 18:15:32 ; Search time 90 Seconds
(without alignments)
2112.009 Million cell updates/sec

Title: US-09-581-528E-3

Perfect score: 2339
Sequence: 1 MFEIRAPAPLSTFQNAQMSBDS.....ATDYLVQPFMDQLAFHQFYI 467

Scoring table: BLOSUM62
Gapco 10.0, Gapext 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2240	93.6	467	16	US-10-811-199-2
3	2239	93.6	467	9	US-09-754-949-4
4	2239	93.6	467	9	US-09-878-454A-3
5	2239	93.6	467	9	US-09-895-035-14
6	2239	93.6	467	13	US-10-071-900-1
7	2239	93.6	467	14	US-10-221-254-4
8	2239	93.6	467	14	US-10-180-781-3
9	2239	93.6	467	15	US-10-417-422-4
10	2239	93.6	467	16	US-10-888-004-14
11	2239	93.6	467	17	US-10-221-291-3

12	2234	93.4	467	9	US-09-785-474-2	Sequence 2, Appli
13	2229	93.1	467	9	US-09-785-474-32	Sequence 32, Appli
14	2229	93.1	467	10	US-09-896-621B-4	Sequence 4, Appli
15	2227	93.1	467	10	US-09-896-621B-5	Sequence 5, Appli
16	2224	92.9	467	9	US-09-785-474-30	Sequence 30, Appli
17	2222	92.9	467	9	US-09-785-474-28	Sequence 28, Appli
18	2217	92.6	467	10	US-09-896-621B-6	Sequence 6, Appli
19	2210	92.4	463	9	US-09-895-035-12	Sequence 12, Appli
20	2210	92.4	463	16	US-10-888-004-12	Sequence 4, Appli
21	2207	92.2	467	9	US-09-785-474-4	Sequence 5, Appli
22	2198	91.4	467	14	US-10-293-000-5	Sequence 2, Appli
23	1468	61.3	448	9	US-09-878-454A-1	Sequence 1, Appli
24	1468	61.3	448	13	US-10-071-900-2	Sequence 2, Appli
25	1468	61.3	448	14	US-10-293-000-6	Sequence 6, Appli
26	1468	61.3	448	14	US-10-180-781-2	Sequence 2, Appli
27	1463	61.1	448	16	US-10-811-199-9	Sequence 9, Appli
28	1460	61.0	448	9	US-09-754-949-6	Sequence 6, Appli
29	1460	61.0	448	14	US-10-221-254-6	Sequence 6, Appli
30	1460	61.0	448	15	US-10-417-422-6	Sequence 5, Appli
31	1460	61.0	448	17	US-10-221-291-5	Sequence 10, Appli
32	1450	60.6	448	10	US-09-896-621B-10	Sequence 11, Appli
33	1448	60.5	448	10	US-09-896-621B-11	Sequence 12, Appli
34	1438	60.1	448	10	US-09-896-621B-12	Sequence 1, Appli
35	985.5	41.2	461	16	US-10-811-199-1	Sequence 6, Appli
36	985.5	41.2	461	16	US-10-811-199-6	Sequence 1, Appli
37	717.5	30.0	180	9	US-09-895-035-1	Sequence 1, Appli
38	717.5	30.0	180	16	US-10-888-004-1	Sequence 8, Appli
39	591.5	24.7	354	9	US-09-823-153-8	Sequence 8, Appli
40	591.5	24.7	354	16	US-10-713-981-8	Sequence 60796, A
41	562.5	23.5	478	15	US-10-425-114-60796	Sequence 352586, A
42	562.5	23.5	479	16	US-10-425-114-352586	Sequence 47501, A
43	562.5	23.5	491	15	US-10-425-114-47501	Sequence 166498, A
44	543.5	22.7	436	16	US-10-437-963-166498	Sequence 3, Appli
45	507	21.2	157	16	US-10-811-199-3	

ALIGNMENTS

RESULT 1
US-10-957-311-3
Sequence 3, Application US/10957311
Publication No. US20050076400A1
GENERAL INFORMATION:
APPLICANT: CASAS LOUZA, Cely
APPLICANT: BENOIT, Patrick
APPLICANT: PRADIER, Laurent
APPLICANT: TREMP, Gunter
APPLICANT: IRIER, Jean-Michel
APPLICANT: BLANCHARD, Veronique
TITLE OF INVENTION: TRANSGENIC ANIMALS EXHIBITING MAJOR DISORDERS RELATED TO
FILE REFERENCE: FRAV2003/0027 US NP
CURRENT APPLICATION NUMBER: US/10/957,311
CURRENT FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/523,397
PRIOR FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: FR 0311578
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Artificialat
FEATURE:
OTHER INFORMATION: Murine P51 Protein with Mutations M233T and I235P
US-10-957-311-3
Query Match 99.2% Score 2374; DB 17; Length 467;
Best Local Similarity 99.1% Pred. No. 1.3e-203;
Matches 463; Conservative 2; Mismatches 2; Gaps 0;

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OM protein - protein search, using sw model

Run on: September 26, 2005, 16:28:22 / Search time 31 Seconds
(without alignments)
1124.552 Million cell updates/sec

Title: US-09-581-528E-3

Perfect score: 2393

Sequence: 1 MTEIPAPLSTYFQNMQSEDS.....ATDYLVQFMDQLAHQFYI 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
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2	2387	99.7	467 3	US-08-496-841C-136 Sequence 136, App
3	2366	98.9	465 4	US-09-496-239A-18 Sequence 18, Appl
4	2337	97.7	467 2	US-08-967-101-4 Sequence 4, Appl
5	2337	97.7	467 2	US-08-592-541-4 Sequence 4, Appl
6	2337	97.7	467 3	US-09-124-698-4 Sequence 4, Appl
7	2337	97.7	467 3	US-09-127-480-4 Sequence 4, Appl
8	2337	97.7	467 3	US-08-496-841C-4 Sequence 4, Appl
9	2337	97.7	467 3	US-09-124-523-4 Sequence 4, Appl
10	2337	97.7	467 4	US-09-636-796A-4 Sequence 4, Appl
11	2337	97.7	467 4	US-08-431-048F-4 Sequence 4, Appl
12	2333.5	97.5	465 3	US-08-788-231A-17 Sequence 17, Appl
13	2240	93.6	467 4	US-09-043-944-2 Sequence 2, Appl
14	2239	93.6	467 2	US-08-967-101-134 Sequence 134, App
15	2239	93.6	467 2	US-08-923-454A-134 Sequence 134, App
16	2239	93.6	467 3	US-08-923-454A-10 Sequence 10, Appl
17	2239	93.6	467 3	US-08-670-964-2 Sequence 2, Appl
18	2239	93.6	467 3	US-08-888-077A-2 Sequence 2, Appl
19	2239	93.6	467 3	US-09-124-698-134 Sequence 134, App
20	2239	93.6	467 3	US-09-127-480-134 Sequence 134, App
21	2239	93.6	467 3	US-08-496-841C-134 Sequence 134, App
22	2239	93.6	467 3	US-08-832-867-3 Sequence 3, Appl
23	2239	93.6	467 3	US-09-272-725A-1 Sequence 1, Appl
24	2239	93.6	467 3	US-09-124-523-134 Sequence 134, App
25	2239	93.6	467 4	US-09-375-318-3 Sequence 3, Appl
26	2239	93.6	467 4	US-09-636-796A-134 Sequence 134, App
27	2239	93.6	467 4	US-09-895-035-14 Sequence 14, Appl

28	2239	93.6	467 4	US-09-501-171-1 Sequence 1, Appl
29	2239	93.6	467 4	US-09-949-016-5873 Sequence 5873, Ap
30	2239	93.6	487 4	US-09-949-016-9173 Sequence 9173, Ap
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35	2233	93.3	467 2	US-08-592-541-2 Sequence 2, Appl
36	2233	93.3	467 3	US-09-124-698-2 Sequence 2, Appl
37	2233	93.3	467 3	US-09-127-480-2 Sequence 2, Appl
38	2233	93.3	467 3	US-08-496-841C-2 Sequence 2, Appl
39	2233	93.3	467 4	US-09-124-523-2 Sequence 2, Appl
40	2233	93.3	467 4	US-09-636-796A-2 Sequence 2, Appl
41	2233	93.3	467 4	US-08-431-048F-2 Sequence 2, Appl
42	2229	93.1	467 3	US-08-706-344C-32 Sequence 32, Appl
43	2229	93.1	467 4	US-09-896-621B-4 Sequence 4, Appl
44	2227	93.1	467 4	US-09-896-621B-5 Sequence 5, Appl
45	2224	92.9	467 3	US-08-706-344C-30 Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-888-077A-17
Sequence 17, Application US/08888077A
Patent No. 6020143
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLUP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-888-077A-17

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Best Local Similarity 99.6%, Pred. No. 2.8e-235;
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